

PCT

RAW SEQUENCE LISTING DATE: 02/05/2001
 PATENT APPLICATION: US/09/720,841 TIME: 16:34:36

Input Set : A:\5787585.txt
 Output Set: N:\CRF3\02052001\I720841.raw

3 <110> APPLICANT: Biotica Technology Limited
 4 Leadlay, Peter F
 5 Pfizer, Inc.
 6 Staunton, James
 7 Cortes, Jesus
 8 McArthur, Hamish AI
 10 <120> TITLE OF INVENTION: Polyketides and their synthesis
 12 <130> FILE REFERENCE: IS/CP5787585
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/720,841
 C--> 15 <141> CURRENT FILING DATE: 2000-12-29
 17 <150> PRIOR APPLICATION NUMBER: CB 9814006.4
 18 <151> PRIOR FILING DATE: 1998-06-29
 20 <160> NUMBER OF SEQ ID NOS: 53
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 398
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Streptomyces sp. C5
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 33 Ala Ile Trp Asp Ala Val Leu Asn Gly Arg Asn Gly Ile Gly Pro Leu
 34 20 25 30
 36 Arg Arg Phe Ala Asp Asp Gly Arg Leu Gly Arg Leu Ala Gly Glu Val
 37 35 40 45
 39 Ser Asp Phe Val Pro Glu Asp His Leu Pro Lys Arg Leu Leu Val Gln
 40 50 55 60
 42 Thr Asp Pro Met Thr Gln Met Thr Ala Leu Ala Ala Glu Trp Ala
 43 65 70 75 80
 45 Leu Arg Glu Ala Gly Cys Ala Pro Ser Ser Pro Leu Glu Ala Gly Val
 46 85 90 95
 48 Ile Thr Ala Ser Ala Ser Gly Gly Phe Ala Ser Gly Gln Arg Glu Leu
 49 100 105 110
 51 Gln Asn Leu Trp Ser Lys Gly Pro Ala His Val Ser Ala Tyr Met Ser
 52 115 120 125
 54 Phe Ala Trp Phe Tyr Ala Val Asn Thr Gly Gln Ile Ala Ile Arg His
 55 130 135 140
 57 Asp Leu Arg Gly Pro Val Gly Val Val Val Ala Glu Gln Ala Gly Gly
 58 145 150 155 160
 60 Leu Asp Ala Leu Ala His Ala Arg Arg Lys Val Arg Gly Gly Ala Glu
 61 165 170 175
 63 Leu Ile Val Ser Gly Ala Met Asp Ser Ser Leu Cys Pro Tyr Gly Met
 64 180 185 190
 66 Ala Ala Gln Val Arg Ser Gly Arg Leu Ser Gly Ser Asp Asp Pro Thr
 67 195 200 205
 69 Ala Gly Tyr Leu Pro Phe Asp Arg Arg Ala Ala Gly His Val Pro Gly
 70 210 215 220

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72 Glu Gly Gly Ala Ile Leu Ala Val Glu Asp Ala Glu Arg Val Ala Glu
 73 225 230 235 240
 75 Arg Gly Gly Lys Val Tyr Gly Ser Ile Ala Gly Thr Ala Ser Phe Asp
 76 245 250 255
 78 Pro Pro Pro Gly Ser Gly Arg Pro Ser Ala Leu Ala Arg Ala Val Glu
 79 260 265 270
 81 Thr Ala Leu Ala Asp Ala Gly Leu Asp Arg Ser Asp Ile Ala Val Val
 82 275 280 285
 84 Phe Ala Asp Gly Ala Ala Val Gly Glu Leu Asp Val Ala Glu Ala Glu
 85 290 295 300
 87 Ala Leu Ala Ser Val Phe Gly Pro His Arg Val Pro Val Thr Val Pro
 88 305 310 315 320
 90 Lys Thr Leu Thr Gly Arg Leu Tyr Ser Gly Ala Gly Pro Leu Asp Val
 91 325 330 335
 93 Ala Thr Gly Leu Ala Leu Arg Asp Glu Val Val Pro Ala Thr Gly
 94 340 345 350
 96 His Val His Pro Asp Pro Asp Leu Pro Leu Asp Val Val Thr Gly Arg
 97 355 360 365
 99 Pro Arg Ala Met Ala Asp Ala Arg Ala Leu Val Val Ala Arg Gly
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 108 <211> LENGTH: 425
 109 <212> TYPE: PRT
 110 <213> ORGANISM: Streptomyces peucetius
 112 <400> SEQUENCE: 2
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 114 1 5 10 15
 116 Pro Ala Gly Arg Arg Gly Leu Arg Gly Arg Ala Val Val Thr Gly Leu
 117 20 25 30
 119 Gly Ile Val Ala Pro Asn Gly Leu Gly Val Gly Ala Tyr Trp Asp Ala
 120 35 40 45
 122 Val Leu Asn Gly Arg Asn Gly Ile Gly Pro Leu Arg Arg Phe Thr Gly
 123 50 55 60
 125 Asp Gly Arg Leu Gly Arg Leu Ala Gly Glu Val Ser Asp Phe Val Pro
 126 65 70 75 80
 128 Glu Asp His Leu Pro Lys Arg Leu Leu Ala Glu Thr Asp Pro Met Thr
 129 85 90 95
 131 Gln Tyr Ala Leu Ala Ala Glu Trp Ala Leu Arg Glu Ser Gly Cys
 132 100 105 110
 134 Ser Pro Ser Ser Pro Leu Glu Ala Gly Val Ile Thr Ala Ser Ala Ser
 135 115 120 125
 137 Gly Gly Phe Ala Phe Gly Gln Arg Glu Leu Gln Asn Leu Trp Ser Lys
 138 130 135 140
 140 Gly Pro Ala His Val Ser Ala Tyr Met Ser Phe Ala Trp Phe Tyr Ala
 141 145 150 155 160
 143 Val Asn Thr Gly Gln Ile Ala Ile Arg His Asp Leu Arg Gly Pro Val
 144 165 170 175

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146 Gly Val Val Val Ala Glu Gln Ala Gly Gly Leu Asp Ala Leu Ala His
 147 180 185 190
 149 Ala Arg Arg Lys Val Arg Gly Gly Ala Glu Leu Ile Val Ser Gly Ala
 150 195 200 205
 152 Val Asp Ser Ser Leu Cys Pro Tyr Gly Met Ala Ala Gln Val Lys Ser
 153 210 215 220
 155 Gly Arg Leu Ser Gly Ser Asp Asn Pro Thr Ala Gly Tyr Leu Pro Phe
 156 225 230 235 240
 158 Asp Arg Arg Ala Ala Gly His Val Pro Gly Glu Gly Ala Ile Leu
 159 245 250 255
 161 Thr Val Glu Asp Ala Glu Arg Ala Ala Glu Arg Gly Ala Lys Val Tyr
 162 260 265 270
 164 Gly Ser Ile Ala Gly Tyr Gly Ala Ser Phe Asp Pro Pro Pro Gly Ser
 165 275 280 285
 167 Gly Arg Pro Ser Ala Leu Ala Arg Ala Val Glu Thr Ala Leu Ala Asp
 168 290 295 300
 170 Ala Gly Leu Asp Gly Ser Asp Ile Ala Val Val Phe Ala Asp Gly Ala
 171 305 310 315 320
 173 Ala Val Pro Glu Leu Asp Ala Ala Glu Ala Glu Ala Leu Ala Ser Val
 174 325 330 335
 176 Phe Gly Pro Arg Arg Val Pro Val Thr Val Pro Lys Thr Leu Thr Gly
 177 340 345 350
 179 Arg Leu Tyr Ser Gly Ala Gly Pro Leu Asp Val Ala Thr Ala Leu Leu
 180 355 360 365
 182 Ala Leu Arg Asp Glu Val Val Pro Ala Thr Ala His Val Asp Pro Asp
 183 370 375 380
 185 Pro Asp Leu Pro Leu Asp Val Val Thr Gly Arg Pro Arg Ser Leu Ala
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 188 Asp Ala Arg Ala Ala Leu Leu Val Ala Arg Gly Tyr Gly Gly Phe Asn
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 198 <212> TYPE: PRT
 199 <213> ORGANISM: Streptomyces coelicolor
 201 <400> SEQUENCE: 3
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 205 Gly Leu Ala Pro Tyr Trp Ser Ala Val Leu Asp Gly Arg His Gly Leu
 206 20 25 30
 208 Gly Pro Val Thr Arg Phe Asp Val Ser Arg Tyr Pro Ala Thr Leu Ala
 209 35 40 45
 211 Gly Gln Ile Asp Asp Phe His Ala Pro Asp His Ile Pro Gly Arg Leu
 212 50 55 60
 214 Leu Pro Gln Thr Asp Pro Ser Thr Arg Leu Ala Leu Thr Ala Ala Asp
 215 65 70 75 80
 217 Trp Ala Leu Gln Asp Ala Lys Ala Asp Pro Glu Ser Leu Thr Asp Tyr
 218 85 90 95

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220 Asp Met Gly Val Val Thr Ala Asn Ala Cys Gly Gly Phe Asp Phe Thr
 221 100 105 110
 223 His Arg Glu Phe Arg Lys Leu Trp Ser Glu Gly Pro Lys Ser Val Ser
 224 115 120 125
 226 Val Tyr Glu Ser Phe Ala Trp Phe Tyr Ala Val Asn Thr Gly Gln Ile
 227 130 135 140
 229 Ser Ile Arg His Gly Met Arg Gly Pro Ser Ser Ala Leu Val Ala Glu
 230 145 150 155 160
 232 Gln Ala Gly Gly Leu Asp Ala Leu Gly His Ala Arg Arg Thr Ile Arg
 233 165 170 175
 235 Arg Gly Thr Pro Leu Val Val Ser Gly Gly Val Asp Ser Ala Leu Asp
 236 180 185 190
 238 Pro Trp Gly Trp Val Ser Gln Ile Ala Ser Gly Arg Ile Ser Thr Ala
 239 195 200 205
 241 Thr Asp Pro Asp Arg Ala Tyr Leu Pro Phe Asp Glu Arg Ala Ala Gly
 242 210 215 220
 244 Tyr Val Pro Gly Glu Gly Ala Ile Leu Val Leu Glu Asp Ser Ala
 245 225 230 235 240
 247 Ala Ala Glu Ala Arg Gly Arg His Asp Ala Tyr Gly Glu Leu Ala Gly
 248 245 250 255
 250 Cys Ala Ser Thr Phe Asp Pro Ala Pro Gly Ser Gly Arg Pro Ala Gly
 251 260 265 270
 253 Leu Glu Arg Ala Ile Arg Leu Ala Leu Asn Asp Ala Gly Thr Gly Pro
 254 275 280 285
 256 Glu Asp Val Asp Val Val Phe Ala Asp Gly Ala Gly Val Pro Glu Leu
 257 290 295 300
 259 Asp Ala Ala Glu Ala Arg Ala Ile Gly Arg Val Phe Gly Arg Glu Gly
 260 305 310 315 320
 262 Val Pro Val Thr Val Pro Lys Thr Thr Gly Arg Leu Tyr Ser Gly
 263 325 330 335
 265 Gly Gly Pro Leu Asp Val Val Thr Ala Leu Met Ser Leu Arg Glu Gly
 266 340 345 350
 268 Val Ile Ala Pro Thr Ala Gly Val Thr Ser Val Pro Arg Glu Tyr Gly
 269 355 360 365
 271 Ile Asp Leu Val Leu Gly Glu Pro Arg Ser Thr Ala Pro Arg Thr Ala
 272 370 375 380
 274 Leu Val Leu Ala Arg Gly Arg Trp Gly Phe Asn Ser Ala Ala Val Leu
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 277 Arg Arg Phe Ala Pro Thr Pro
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 283 <211> LENGTH: 403
 284 <212> TYPE: PRT
 285 <213> ORGANISM: Saccharopolyspora hirsuta
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 291 Gly Ala Asp Asp His Trp Ala Ala Thr Leu Lys Gly Arg His Gly Ile
 292 20 25 30

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294 Ser Arg Leu Ser Arg Phe Asp Pro Thr Gly Tyr Pro Ala Glu Leu Ala
 295 35 40 45
 297 Gly Gln Val Leu Asp Phe Asp Ala Thr Glu His Leu Pro Lys Arg Leu
 298 50 55 60
 300 Leu Pro Gln Thr Asp Val Ser Thr Arg Phe Ala Leu Ala Ala Ala Ala
 301 65 70 75 80
 303 Trp Ala Ile Ala Asp Ala Glu Val Asp Pro Ala Glu Leu Pro Glu Tyr
 304 85 90 95
 306 Gly Thr Gly Val Ile Thr Ser Asn Ala Thr Gly Gly Phe Glu Phe Thr
 307 100 105 110
 309 His Arg Glu Phe Arg Lys Leu Trp Ala Gin Gly Pro Glu Phe Val Ser
 310 115 120 125
 312 Val Tyr Glu Ser Phe Ala Trp Phe Tyr Ala Val Asn Thr Gly Gln Ile
 313 130 135 140
 315 Ser Ile Arg His Gly Leu Arg Gly Pro Gly Ser Val Leu Val Ala Glu
 316 145 150 155 160
 318 Gln Ala Gly Gly Leu Asp Ala Val Gly His Gly Gly Ala Val Arg Asn
 319 165 170 175
 321 Gly Thr Pro Met Val Val Thr Gly Gly Val Asp Ser Ser Phe Asp Pro
 322 180 185 190
 324 Trp Gly Trp Val Ser His Val Ser Ser Gly Arg Val Ser Arg Ala Thr
 325 195 200 205
 327 Asp Pro Gly Arg Ala Tyr Leu Pro Phe Asp Val Ala Ala Asn Gly Tyr
 328 210 215 220
 330 Val Pro Gly Glu Gly Ala Ile Leu Leu Glu Asp Ala Glu Ser
 331 225 230 235 240
 333 Ala Lys Ala Arg Gly Ala Thr Gly Tyr Gly Glu Ile Ala Gly Tyr Ala
 334 245 250 255
 336 Ala Thr Phe Asp Pro Ala Pro Gly Ser Glu Arg Pro Pro Ala Leu Arg
 337 260 265 270
 339 Arg Ala Ile Glu Leu Ala Leu Ala Asp Ala Glu Leu Arg Pro Glu Gln
 340 275 280 285
 342 Val Asp Val Val Phe Ala Asp Ala Ala Gly Val Ala Glu Leu Asp Ala
 343 290 295 300
 345 Ile Glu Ala Ala Ala Ile Arg Glu Leu Phe Gly Pro Ser Gly Val Pro
 346 305 310 315 320
 348 Val Thr Ala Pro Lys Thr Met Thr Gly Arg Leu Tyr Ser Gly Gly Gly
 349 325 330 335
 351 Pro Leu Asp Leu Val Ala Ala Leu Leu Ala Ile Arg Asp Gly Val Ile
 352 340 345 350
 354 Pro Pro Thr Val His Thr Ala Gln Pro Val Pro Glu His Gln Ile Asp
 355 355 360 365
 357 Leu Val Thr Gly Asp Pro Arg His Gln Gln Leu Gly Thr Ala Leu Val
 358 370 375 380
 360 Leu Ala Arg Gly Lys Trp Gly Phe Asn Ser Ala Val Val Val Arg Gly
 361 385 390 395 400
 363 Val Thr Gly
 368 <210> SEQ ID NO: 5
 369 <211> LENGTH: 415

VERIFICATION SUMMARY
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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date